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53. The plant cell of claim 52, wherein said fourth coding sequence comprises at least a portion of the nucleotide sequence set forth in SEQ ID NO: 24.

5 54. The plant cell of claim 52 further comprising in its genome a fifth DNA construct comprising a promoter that drives expression in a plant cell operably linked to a fifth coding sequence, wherein said fifth coding sequence encodes an NADH kinase or an NAD⁺ kinase and said fifth coding sequence is operably linked to a nucleotide sequence encoding a peroxisome-targeting signal.

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55. The plant cell of claim 54, wherein said fifth coding sequence comprises at least a portion of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 25-27.

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56. A plant cell genetically manipulated to produce polyhydroxyalkanoate in its peroxisomes, said plant cell comprising in its genome:

a stably integrated first DNA construct comprising a promoter that drives expression in a plant cell operably linked to a first coding sequence, wherein said first coding sequence encodes a polyhydroxyalkanoate synthase and is operably linked to a nucleotide sequence encoding a peroxisome-targeting signal;

a stably integrated second DNA construct comprising a promoter that drives expression in a plant cell operably linked to a second coding sequence, wherein said second coding sequence encodes an acetyl-CoA:acetyl transferase and is operably linked to a nucleotide sequence encoding a peroxisome-targeting signal; and

20 25 a stably integrated third DNA construct comprising a promoter that drives expression in a plant cell operably linked to a third coding sequence, wherein said third coding sequence is operably linked to a nucleotide sequence encoding a peroxisome-targeting signal and said third coding sequence is selected from the group consisting of:

30 (a) a nucleotide sequence encoding a 3-ketoacyl-CoA reductase that is capable of utilizing NADH;
(b) a nucleotide sequence set forth in SEQ ID NO: 3;
(c) a nucleotide sequence set forth in SEQ ID NO: 22;

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(d) the nucleotide sequence set forth in SEQ ID NO: 1;

(e) a nucleotide sequence encoding a multifunctional protein-2, wherein the hydratase activity of said multifunctional protein has been eliminated; and

5 (f) the nucleotide sequence set forth in SEQ ID NO: 6.

57. The plant cell of claim 56, wherein said second coding sequence comprises at least a portion of the nucleotide sequence set forth in SEQ ID NO: 24.

10 58. A plant cell genetically manipulated for the synthesis in its peroxisomes of at least one intermediate molecule in polyhydroxyalkanoate synthesis, said plant cell comprising in its genome at least one stably incorporated DNA construct comprising a coding sequence for an enzyme involved in the synthesis of said intermediate molecule, said coding sequence operably linked to a promoter that drives expression in a plant cell and to a nucleotide sequence encoding a peroxisome-targeting signal, wherein said coding sequence is selected from the group consisting of:

(a) a nucleotide sequence encoding a 2-enoyl-CoA hydratase that is capable of catalyzing the synthesis of R-(ω)-3-hydroxyacyl-CoA ;

20 (b) a nucleotide sequence set forth in SEQ ID NO: 21;

(c) a nucleotide sequence comprising the 2-enoyl-CoA hydratase domain of a multifunctional protein-2.

(d) a nucleotide sequence set forth in SEQ ID NO: 4;

25 (e) a nucleotide sequence set forth in SEQ ID NO: 1;

(f) a nucleotide sequence encoding a multifunctional protein-2, wherein the dehydrogenase activity of said multifunctional protein has been eliminated; and

(g) a nucleotide sequence encoding a 3-ketoacyl-CoA reductase that is capable of utilizing NADH;

30 (h) a nucleotide sequence set forth in SEQ ID NO: 3;

(i) a nucleotide sequence set forth in SEQ ID NO: 22;

(j) the nucleotide sequence set forth in SEQ ID NO: 1;

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- (k) a nucleotide sequence encoding a multifunctional protein-2, wherein the hydratase activity of said multifunctional protein has been eliminated; and
- (l) the nucleotide sequence set forth in SEQ ID NO: 6.

§

59. The plant cell of claim 58, wherein said intermediate molecule is an R-(*-*)-3-hydroxyacyl-CoA or a 3-ketoacyl-CoA.

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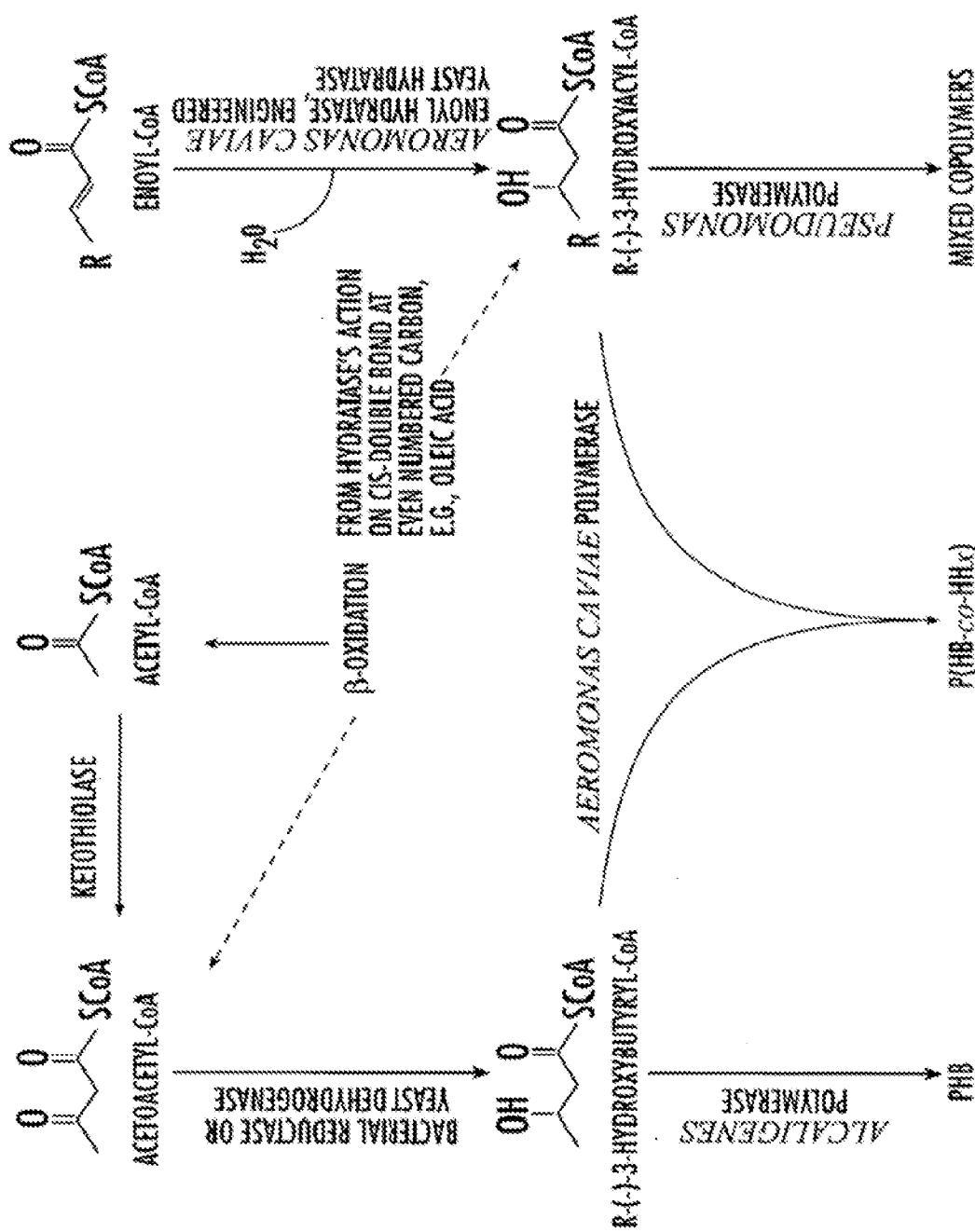
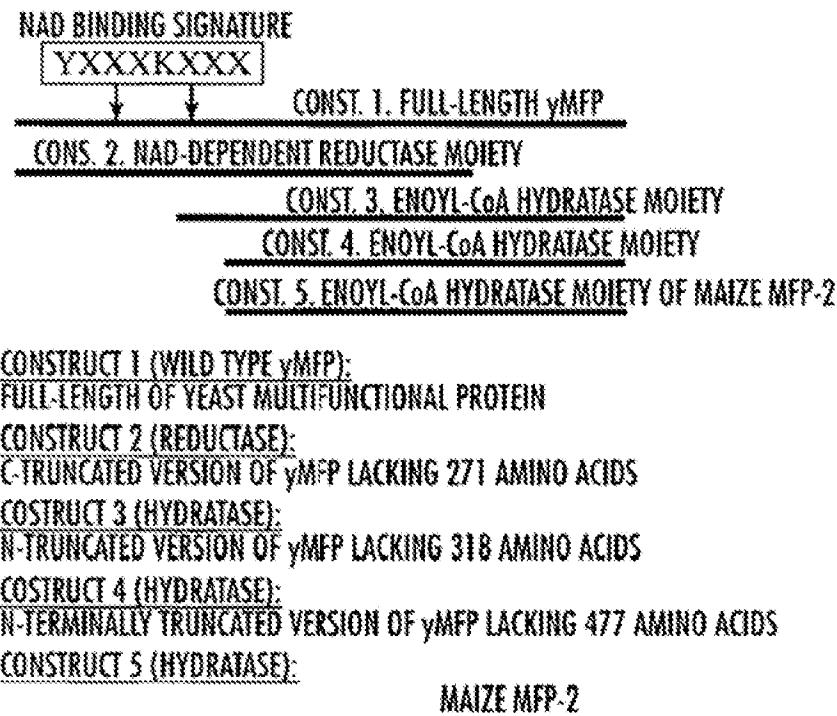


FIG. 1.

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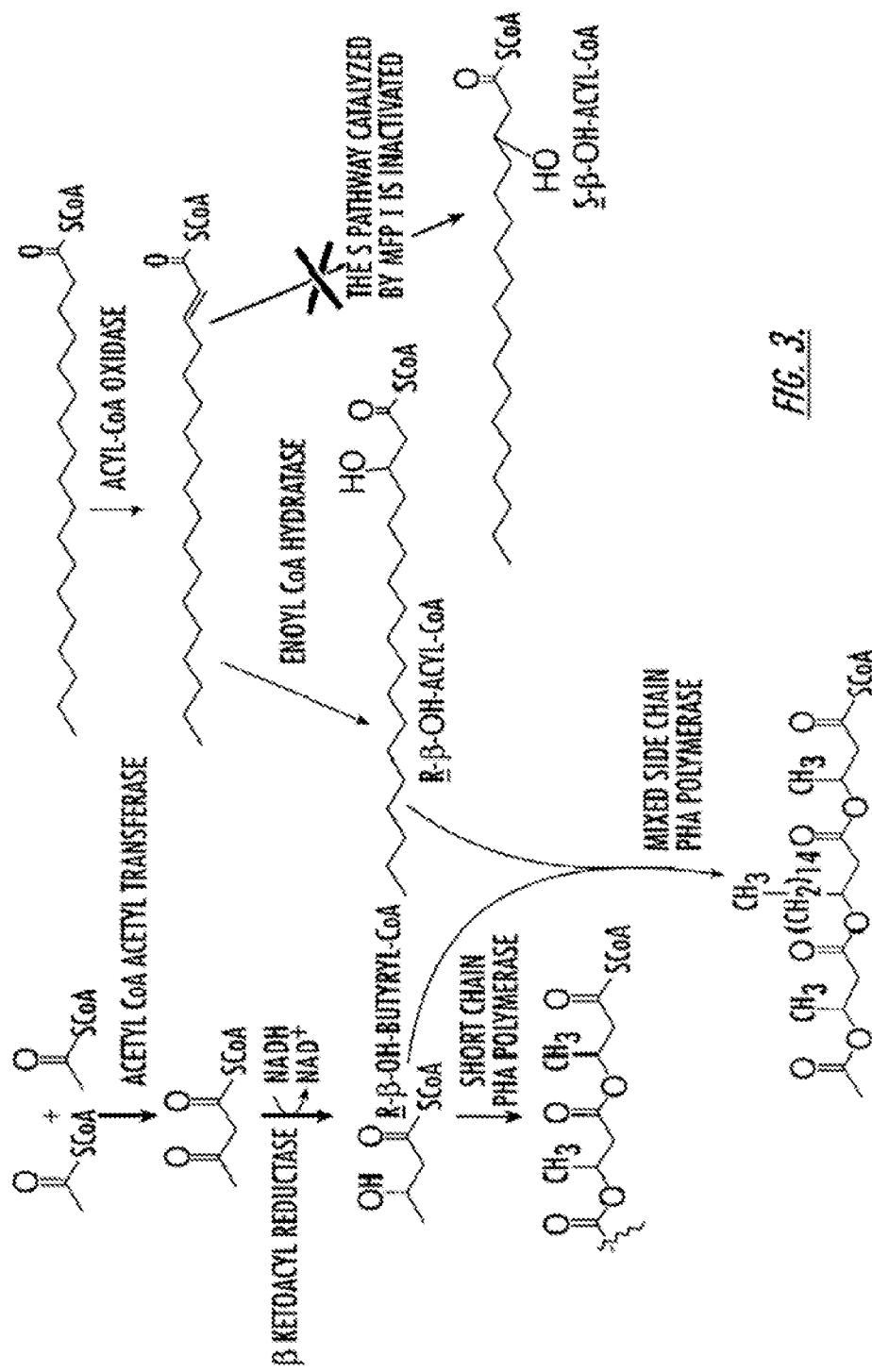
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FIG. 2.

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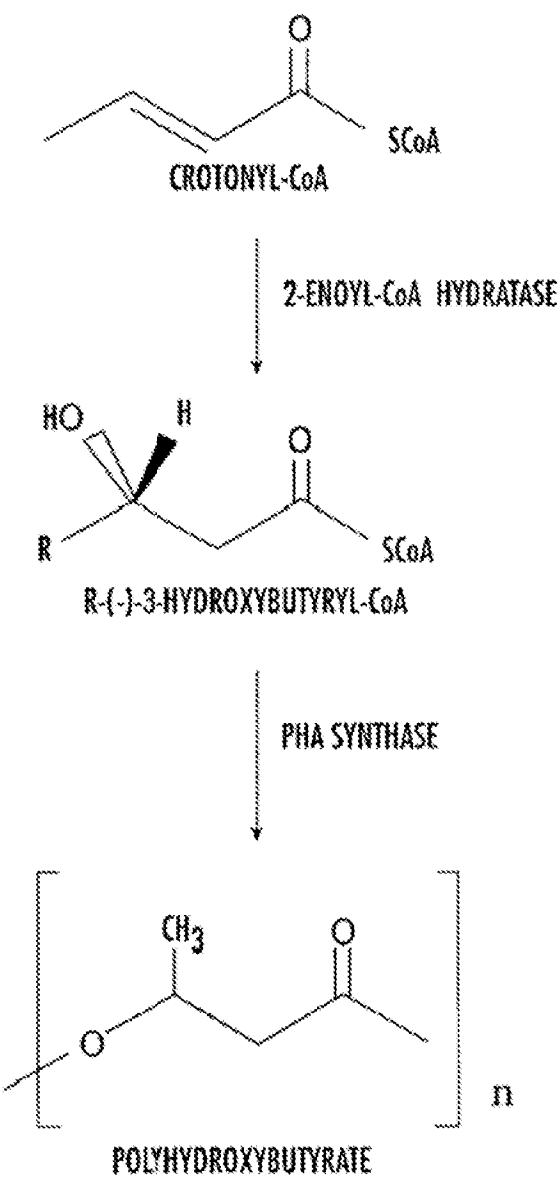


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FIG. 4.

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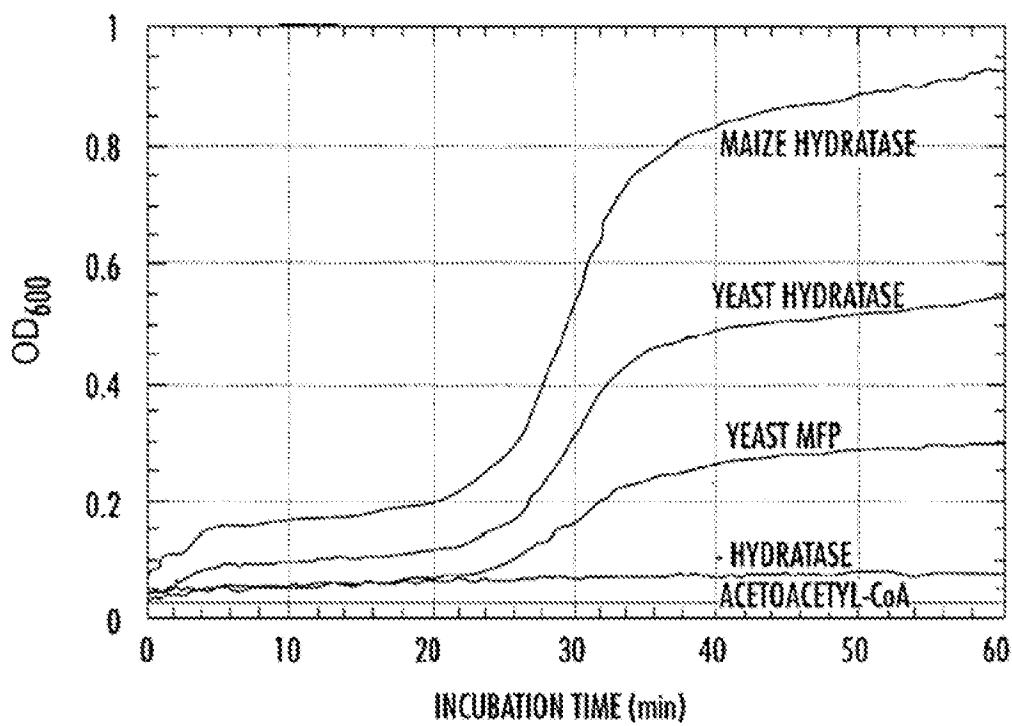


FIG. 5.

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SEQUENCE LISTING

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Li, Chun Ping
Dong, Jian G
Hitz, William D
Liebergesell, Matthias
Dhugga, Kanwarpal S
Briggs, Kristen K

<120> PRODUCTION OF POLYHYDROXYALKANOATE IN PLANTS

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<170> PatentIn Ver. 2.1

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agccatcgacat tccctctttc gtctcttaca atgtccaga caccactccg actttgcggg 180
caaccctgtcg acagcgacga ggccatcgat aaggcatacg ggcacggcgg cc atg gcg 238
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acc agc tcc aaa ccc gcc gcg ccc gtg gac ccc atg gtc gtg ctc gcc 286
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5 10 15

cac gag ttc ccc gag gtg tcc ttc gac tac gac gag agg gat gta gcg 334
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20 25 30

tta tac gcg ctc ggg gtt ggt gcc tgc ggc gat gac gcc gtc gac gag 382
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35 40 45 50

ccg gcg ctt cac ttc gtg tac cac egg gat ggg cag cca csc att aag 430
Lys Glu Leu His Phe Val Tyr His Arg Asp Gly Gln Pro His Ile Lys
55 60 65

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70	75
	80
ctt gga ttt gtt gat gtg cct ggc ctt aac ttt gat gca aac aac ctt cta	526
Leu Gly Phe Val Asp Val Pro Gly Leu Asn Phe Asp Ala Ser Leu Leu	
85	90
	95
ctg ctt ggt caa caa tac atc gag atc tat agg cca atc cct tcc tat	574
Leu His Gly Gln Gln Tyr Ile Glu Ile Tyr Arg Pro Ile Pro Ser Tyr	
100	105
	110
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Val Ser Val Val Asn Arg Val Lys Val Val Gly Leu His Asp Lys Gly	
115	120
	125
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aaa gca act att ctt gag ctc gaa act acc aca aag ctc aaa gag tca	670
Lys Ala Thr Ile Leu Glu Leu Thr Thr Ser Leu Lys Glu Ser	
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Gly Glu Ile Leu Cys Met Asn Arg Ser Thr Ile Tyr Leu Arg Gly Ala	
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Ala Asn Gln Val Ser Arg Ile Ser Ile Pro Asn Ser Ala Pro Ser Ala	
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	205
	210
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Ser Gly Asp Tyr Asn Pro Leu His Ser Asp Pro Asp Ile Ala Gln Leu	
215	220
	225
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Ala Gly Phe Thr Arg Pro Ile Leu His Gly Leu Cys Thr Leu Gly Phe	
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Ala Ala Arg Ala Val Ile Lys Ser Phe Cys Asn Gly Glu Pro Thr Ala	
245	250
	255
gtg aag agc atc ttc ggc cgt ttg ctt ctg cac gtc tac ccc ggg gaa	1054
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	270
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	285
	290
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295	300
	305

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Asp Glu Lys Glu Leu His Phe Val Tyr His Arg Asp Gly Gln Pro His
50 55 60

Ile Lys Thr Leu Pro Thr Phe Val Ser Leu Phe Pro Asn Lys Asn Ser
65 70 75 80

Asn Gly Leu Gly Phe Val Asp Val Pro Gly Leu Asn Phe Asp Ala Ser
85 90 95

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Ser Tyr Val Ser Val Val Asn Arg Val Lys Val Val Gly Leu His Asp
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Lys Gly Lys Ala Thr Ile Leu Glu Leu Glu Thr Thr Ser Leu Lys
130 135 140

Glu Ser Gly Glu Ile Leu Cys Met Asn Arg Ser Thr Ile Tyr Leu Arg
145 150 155 160

Gly Ala Gly Gly Phe Ser Asp Ser Ser Arg Pro Tyr Ser Tyr Ala Thr
165 170 175

Tyr Pro Ala Asn Gln Val Ser Arg Ile Ser Ile Pro Asn Ser Ala Pro
180 185 190

Ser Ala Val Cys Asp Asp Gln Thr Lys Gln Ser Gln Ala Leu Leu Tyr
195 200 205

Arg Leu Ser Gly Asp Tyr Asn Pro Leu His Ser Asp Pro Asp Ile Ala
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Gln Leu Ala Gly Phe Thr Arg Pro Ile Leu His Gly Leu Cys Thr Leu

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Thr Ala Val Lys Ser Ile Phe Gly Arg Phe Leu Leu His Val Tyr Pro			
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Gly Glu Thr Leu Ser Thr Glu Met Trp Leu Asp Gly Gln Lys Val His			
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<223> Nucleotides 4-1566 of SEQ ID NO: 4 corresponds to nucleotides 1381-2943 of SEQ ID NO: 3.

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Gln Arg Val Asp Ile Leu Val Asn Asn Ala Gly Ile Leu Arg Asp Lys
          20           25           30

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cac ctt ttt tcc aca ttt tca ttg tca aaa gca gta tgg cca ata ttt 192
 His Leu Phe Ser Thr Phe Ser Leu Ser Lys Ala Val Trp Pro Ile Phe
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acc ssa cca aag tct gga ttt att atc aat act act act tat acc tca gga 240
 Thr Lys Gln Lys Ser Gly Phe Ile Ile Asn Thr Thr Ser Thr Ser Gly
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att tat ggt aat ttt gga cag gcc sat tat gcc gct gca aea gcc gcc 288
 Ile Tyr Gly Asn Phe Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Ala
 85 90 95

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Ile Ile Val Asn Val Ile Ala Pro His Ala Glu Thr Ala Met Thr Lys			
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Thr Ile Phe Ser Glu Lys Leu Ser Asn His Phe Asp Ala Ser Gln			
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Ser Gly Arg Arg Val Ile Gly Gln Leu Phe Glu Val Gly Gly Trp			
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tgt ggg caa acc aca tgg cca aca agt tcc ggt tat gtt tct tat att aca	576		
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Glu Thr Ile Glu Pro Glu Glu Ile Lys Glu Asn Trp Asn His Ile Thr			
195	200	205	
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tta gga ctt gga tgc aca aca aag ctt aac tac acc tac gag aat	816		
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Thr Leu Ala Lys Ala Val Lys Phe Pro Thr Pro Ile Leu His Gly Leu	
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Cys Thr Leu Gly Ile Ser Ala Lys Ala Leu Phe Glu His Tyr Gly Pro	
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465	470
475	480
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Thr Leu Lys Val Lys Ala Trp Lys Gln Gly Ser Val Val Val Phe Gln	
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495	
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<223> Nucleotides 4-1566 of SEQ ID NO: 4 corresponds to nucleotides 1381-2943 of SEQ ID NO: 3.

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1 S 10

15

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Ser Phe Leu Lys Met Lys Asp Glu Glu Trp Phe Ala Val Leu Lys Val
 35 40 45

His Leu Phe Ser Thr Phe Ser Leu Ser Lys Ala Val Trp Pro Ile Phe
 50 55 60

Thr Lys Gin Lys Ser Gly Phe Ile Ile Asn Thr Thr Ser Thr Ser Gly
 65 70 75 80

Ile Tyr Gly Asn Phe Gly Gln Ala Asn Tyr Ala Ala Lys Ala Ala
 85 90 95

Ile Leu Gly Phe Ser Lys Thr Ile Ala Leu Glu Gly Ala Lys Arg Gly
 100 105 110

Ile Ile Val Asn Val Ile Ala Pro His Ala Glu Thr Ala Met Thr Lys
 115 120 125

Thr Ile Phe Ser Glu Lys Gln Leu Ser Asn His Phe Asp Ala Ser Gln
 130 135 140

Val Ser Pro Leu Val Val Leu Leu Ala Ser Glu Glu Leu Gln Lys Tyr
 145 150 155 160

Ser Gly Arg Arg Val Ile Gly Gln Leu Phe Glu Val Gly Gly Trp
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Cys Gly Gln Thr Arg Trp Gln Arg Ser Ser Gly Tyr Val Ser Ile Lys
 180 185 190

Glu Thr Ile Glu Pro Glu Gln Ile Lys Glu Asn Trp Asn His Ile Thr
 195 200 205

Asp Phe Ser Arg Asn Thr Ile Asn Pro Ser Ser Thr Glu Glu Ser Ser
 210 215 220

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 225 230 235 240

Asp Asp Gly Leu Phe Lys Tyr Thr Thr Lys Asp Cys Ile Leu Tyr Asn
 245 250 255

Leu Gly Leu Gly Cys Thr Ser Lys Glu Leu Lys Tyr Thr Tyr Glu Asn
 260 265 270

Asp Pro Asp Phe Gln Val Leu Pro Thr Phe Ala Val Ile Pro Phe Met
 275 280 285

Gln Ala Thr Ala Thr Leu Ala Met Asp Asn Leu Val Asp Asn Phe Asn
 290 295 300

Tyr Ala Met Leu Leu His Gly Glu Gln Tyr Phe Lys Leu Cys Thr Pro
 305 310 315 320

Thr Met Pro Ser Asn Gly Thr Leu Lys Thr Leu Ala Lys Pro Leu Gln
 325 330 335

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 Thr Tyr Asp Ile Lys Thr Lys Lys Leu Ile Ala Tyr Asn Glu Gly Ser
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 Gly Lys Arg Ala Lys Phe Ala Val Gln Asn Phe Glu Val Pro His Gly
 385 390 395 400
 Lys Val Pro Asp Phe Glu Ala Glu Ile Ser Thr Asn Lys Asp Gln Ala
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 Ala Leu Tyr Arg Leu Ser Gly Asp Phe Asn Pro Leu His Ile Asp Pro
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 Thr Leu Ala Lys Ala Val Lys Phe Pro Thr Pro Ile Leu His Gly Leu
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 Thr Leu Lys Val Lys Ala Trp Lys Gln Gly Ser Val Val Val Phe Gln
 485 490 495
 Thr Ile Asp Thr Thr Arg Asn Val Ile Val Leu Asp Asn Ala Ala Val
 500 505 510
 Lys Leu Ser Gln Ala Lys Ser Lys Leu
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<210> 6
<211> 1887
<212> DNA
<213> *Saccharomyces cerevisiae*

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<223> Nucleotides 1-1887 of SEQ ID NO: 6 corresponds
to nucleotides 241- 2127 of SEQ ID NO: 3.

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Met Pro Gly Asn Leu Ser Phe Lys Asp Arg Val Val Val Ile Thr Gly
 1 5 10 15
 gct gga ggg ggc tta ggt aag gtc tat gca cta gct tac gca agc aga 96
 Ala Gly Gly Leu Gly Lys Val Tyr Ala Leu Ala Tyr Ala Ser Arg
 20 25 30

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ggg gca aaa gtg gtc gtc aat gat cta ggt ggc act ttg ggt ggt tca	144
Gly Ala Lys Val Val Val Asn Asp Leu Gly Thr Leu Gly Gly Ser	
35	40
45	
gga cat aac tcc aea gct gca gac tta gtg gtg gat gag ata aea aea	192
Gly His Asn Ser Lys Ala Ala Asp Leu Val Val Asp Glu Ile Lys Lys	
50	55
60	
gcc gga ggt ata gct gtg gca aat tac gac tct gtt aat gaa aat gga	240
Ala Gly Gly Ile Ala Val Ala Asn Tyr Asp Ser Val Asn Glu Asn Gly	
65	70
75	80
gag aea ata att gaa acg gct ata aea gaa ttc ggc agg gtt gat gta	288
Glu Lys Ile Glu Thr Ala Ile Lys Glu Phe Gly Arg Val Asp Val	
85	90
95	
cta att aac aac gct gga ata tta egg gat gtt tca ttt gca aag atg	336
Leu Ile Asn Asn Ala Gly Ile Leu Arg Asp Val Ser Phe Ala Lys Met	
100	105
110	
aca gaa cgt gag ttt gca tct gtg gta gat gtt cat ttg aca ggt ggc	384
Thr Glu Arg Glu Phe Ala Ser Val Val Asp Val His Ile Thr Gly Gly	
115	120
125	
tat aag cta tcg cgt gct gct tgg cct tat atg cgc tct cag aea ttt	432
Tyr Lys Leu Ser Arg Ala Ala Trp Pro Tyr Met Arg Ser Gln Lys Phe	
130	135
140	
ggt aya atc att aac acc gct tcc cct gcc ggt cta ttt gga aat ttt	480
Gly Arg Ile Ile Asn Thr Ala Ser Pro Ala Gly Leu Phe Gly Asn Phe	
145	150
155	160
ggt caa gct aat tat tca gca gct aea atg ggc tta gtt ggt ttt gog	528
Gly Gln Ala Asn Tyr Ser Ala Ala Lys Met Gly Ile Val Gly Leu Ala	
165	170
175	
gaa acc ctc gcg aag gag ggt ggc aea tcc aac att aat gtt aat tca	576
Glu Thr Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Asn Val Asn Ser	
180	185
190	
att gcg cca ttg gct aya tca cgt atg aca gaa aac gtt tta cca cca	624
Ile Ala Pro Leu Ala Arg Ser Arg Met Thr Glu Asn Val Leu Pro Pro	
195	200
205	
cat atc ttg aea cag tta gga cog gaa aea att gtt ccc tta gta ctc	672
His Ile Leu Lys Gln Leu Gly Pro Glu Lys Ile Val Pro Leu Val Leu	
210	215
220	
tat ttg aca ccc gaa agt acg aea gtg tca aac tcc att ttt gaa ctc	720
Tyr Leu Thr His Glu Ser Thr Lys Val Ser Asn Ser Ile Phe Glu Leu	
225	230
235	240
gct gct gga ttc ttt gga cag ctc aya tgg gag aya tct tct gga caa	768
Aia Ala Gly Phe Phe Gly Gln Leu Arg Trp Glu Arg Ser Ser Gly Gln	
245	250
255	
att ttc aat cca gac ccc aag aca tat act cct gaa gca att tta aat	816
Ile Phe Asn Pro Asp Pro Lys Thr Tyr Thr Pro Glu Ala Ile Leu Asn	
260	265
270	

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aag tgg aag gaa atc aca gac tat agg gac aag cca ttt aac aaa act	864
Lys Trp Lys Glu Ile Thr Asp Tyr Arg Asp Lys Pro Phe Asn Lys Thr	
275	280
285	
cag cat cca tat caa ctc tcc gat tat aat gat tta atc acc aaa gca	912
Gln His Pro Tyr Gln Leu Ser Asp Tyr Asn Asp Leu Ile Thr Lys Ala	
290	295
300	
aaa aaa tta cct ccc aat gaa cca ggc tca gtg aaa atc aag tcc ctt	960
Lys Lys Leu Pro Pro Asn Gln Gly Ser Val Lys Ile Lys Ser Leu	
305	310
315	320
tgc aac aaa gtc gta gta gti aca ggt gca gga ggt ggt ctt ggg aag	1008
Cys Asn Lys Val Val Val Thr Gly Ala Gly Gly Leu Gly Lys	
325	330
335	
tct cat gca atc tgg ttt gca cgg tac ggt gcg aag gta gtt gta aat	1056
Ser His Ala Ile Trp Phe Ala Arg Tyr Gly Ala Lys Val Val Asn	
340	345
350	
gac atc aag gat cct ttt tca gtt gtt gaa gaa ata aat aaa cta tat	1104
Asp Ile Lys Asp Pro Phe Ser Val Val Glu Glu Ile Asn Lys Leu Tyr	
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365	
ggt gaa ggc aca gcc att cca gat tcc cat gat gtc gtc acc gaa gct	1152
Gly Glu Gly Thr Ala Ile Pro Asp Ser His Asp Val Val Thr Gln Ala	
370	375
380	
cct ctc att atc caa act gca ata sgt aag ttt caq aca gta gac atc	1200
Pro Leu Ile Ile Gln Thr Ala Ile Ser Lys Phe Gln Arg Val Asp Ile	
385	390
395	400
405	
ttg gtc aat aac gct att ttg cgt gac aaa tct ttt tta aaa atg	1248
Leu Val Asn Asn Ala Gly Ile Leu Arg Asp Lys Ser Phe Leu Lys Met	
410	415
aaa gat gag gaa tgg ttt gct gtc ctg aaa gtc cad ctt ttt tcc aca	1286
Lys Asp Glu Glu Trp Phe Ala Val Leu Lys Val His Leu Phe Ser Thr	
420	425
430	
tct tca ttg tca aca gca gta tgg cca ata ttt acc aaa caa aag tot	1344
Phe Ser Leu Ser Lys Ala Val Trp Pro Ile Phe Thr Lys Gln Lys Ser	
435	440
445	
gga ttt att atc aat act act tct acc tca gga att tat ggt aat ttt	1382
Gly Phe Ile Ile Asn Thr Thr Ser Thr Ser Gly Ile Tyr Gly Asn Phe	
450	455
460	
gga cag gcc aat tat gcc gct gca aaa gcc gac att tta gga ttc agt	1440
Gly Gln Ala Asn Tyr Ala Ala Lys Ala Ala Ile Leu Gly Phe Ser	
465	470
475	480
aaa act att gca ctg gaa ggt gcc aag aca gga att att gtt aat gtt	1488
Lys Thr Ile Ala Ile Glu Gly Ala Lys Arg Gly Ile Ile Val Asn Val	
485	490
495	
atc gct cct cat gca gaa acg gat atg aca aag act ata ttc tcc gag	1536
Ile Ala Pro His Ala Glu Thr Ala Met Thr Lys Thr Ile Phe Ser Glu	
500	505
510	

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515	520
525	
gtt ttg ttg gca tct gaa gaa cta caa aag tat tct gga aga agg gtt	1632
Val Leu Leu Ala Ser Gln Glu Leu Gln Lys Tyr Ser Gly Arg Arg Val	
530	535
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att ggc caa tta ttc gaa gtt ggc aat ggt tgg tct ggg cca acc aga	1680
Ile Gly Gln Leu Phe Glu Val Gly Gly Trp Cys Gly Gln Thr Arg	
545	550
555	560
tgg caa aca agt tcc ggt tat gtt tct att aca gag act att gaa ccg	1728
Trp Gln Arg Ser Ser Gly Tyr Val Ser Ile Lys Glu Thr Ile Glu Pro	
565	570
575	
gaa gaa att aca gaa aat tgg aac cac atc act gat ttc agt cgc aac	1776
Glu Glu Ile Lys Glu Asn Trp Asn His Ile Thr Asp Phe Ser Arg Asn	
580	585
590	
act atc aac ccg aca tcc aca gag gag tct tct atg gca acc ttg caa	1824
Thr Ile Asn Pro Ser Ser Thr Glu Glu Ser Ser Met Ala Thr Leu Gln	
595	600
605	
gcc gtc caa aca gcg cac tct tca aag gag ttg gat gat ggc tta ttc	1872
Ala Val Glu Lys Ala Ser Ser Lys Glu Leu Asp Asp Gly Leu Phe	
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Lys Tyr Thr Thr Lys	
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<210> 7

<211> 629

<212> FRT

<213> *Saccharomyces cerevisiae*

<223> Nucleotides 1-1887 of SEQ ID NO: 6 corresponds to nucleotides 241- 3127 of SEQ ID NO: 3.

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Ala Gly Gly Leu Gly Lys Val Tyr Ala Leu Ala Tyr Ala Ser Arg	
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35	40
45	

Gly His Asn Ser Lys Ala Ala Asp Leu Val Val Asp Glu Ile Lys Lys	
50	55
60	

Ala Gly Gly Ile Ala Val Ala Asn Tyr Asp Ser Val Asn Glu Asn Gly	
65	70
75	80

Glu Lys Ile Ile Glu Thr Ala Ile Lys Glu Phe Gly Arg Val Asp Val	
85	90
95	

Leu Ile Asn Asn Ala Gly Ile Leu Arg Asp Val Ser Phe Ala Lys Met	
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115	120	125
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130	135	140
Gly Arg Ile Ile Asn Thr Ala Ser Pro Ala Gly Leu Phe Gly Asn Phe		
145	150	155
Gly Gln Ala Asn Tyr Ser Ala Ala Lys Met Gly Leu Val Gly Leu Ala		
165	170	175
Glu Thr Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Asn Val Asn Ser		
180	185	190
Ile Ala Pro Leu Ala Arg Ser Arg Met Thr Glu Asn Val Leu Pro Pro		
195	200	205
Gln Ile Leu Lys Gln Leu Gly Pro Glu Lys Ile Val Pro Leu Val Leu		
210	215	220
Tyr Leu Thr His Glu Ser Thr Lys Val Ser Asn Ser Ile Phe Glu Leu		
225	230	235
Ala Ala Gly Phe Phe Gly Gln Leu Arg Trp Glu Arg Ser Ser Gly Gln		
245	250	255
Ile Phe Asn Pro Asp Pro Lys Thr Tyr Thr Pro Glu Ala Ile Leu Asn		
260	265	270
Lys Trp Lys Glu Ile Thr Asp Tyr Arg Asp Lys Pro Phe Asn Lys Thr		
275	280	285
Gln His Pro Tyr Gln Leu Ser Asp Tyr Asn Asp Leu Ile Thr Lys Ala		
290	295	300
Lys Lys Leu Pro Pro Asn Gln Gln Gly Ser Val Lys Ile Lys Ser Leu		
305	310	315
Cys Asn Lys Val Val Val Val Thr Gly Ala Gly Gly Leu Gly Lys		
325	330	335
Ser His Ala Ile Trp Phe Ala Arg Tyr Gly Ala Lys Val Val Val Asn		
340	345	350
Asp Ile Lys Asp Pro Phe Ser Val Val Glu Glu Ile Asn Lys Leu Tyr		
355	360	365
Gly Glu Gly Thr Ala Ile Pro Asp Ser His Asp Val Val Thr Glu Ala		
370	375	380
Pro Leu Ile Ile Gln Thr Ala Ile Ser Lys Phe Gln Arg Val Asp Ile		
385	390	395
Leu Val Asn Asn Ala Gly Ile Leu Arg Asp Lys Ser Phe Leu Lys Met		
405	410	415
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<210> 8
<211> 6455
<212> DNA
<213> *Pseudomonas clevozensis*

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PCMA 1800/26963

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 <212> DNA
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PCMA 1800/26963

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PCT/US00/26963

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PCMA 1800/26963

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2013-23

2211-2267

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◀212> DNA

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PCMA 1800/26963

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